REMARKS

Entry of the foregoing and favorable reconsideration of the subject application, as amended, pursuant to and consistent with 37 C.F.R. Section 1.112, and in light of the remarks which follow, are respectfully requested.

By the present amendment, claims 1, 12, 30, 32 and 33 have been amended to further clarify the present invention. Claims 8, 16 and 19 have been cancelled. Support for the amended claims appears throughout the specification, e.g., at least on page 7, lines 1 to 10 and page 9, line 22 through page 10, line 33 for claim 12 and at least on page 26, lines 17 to 19 for claims 32 to 34.

Claims 12, 19, and 32 to 34 and claims 13, 17 to 21, 23, 30 and 32 to 34 dependent thereon, have been rejected under 35 U.S.C. §112, second paragraph, as being indefinite.

In rendering this rejection, the Examiner purports that claim 12 does not specify the order of the nucleic acid coding sequence, the promoter and the termination region. This rejection has been rendered moot by the claim amendment.

Applicants submit that the order of the nucleic acid coding sequence, the promoter and the termination region in the recombinant nucleic acid of the present invention is defined in the amended claim 12. Indeed, claim 12 specifies that the plant expressible promoter, the nucleic acid coding for a methyl transferase and the transcription termination sequence are in the recited order.

Applicants set forth that the order of the promoter, the nucleic acid coding sequence and the termination region in the recombinant nucleic acid is well-known with field of the invention. Accordingly, amended claim 12 repeats this specific order of the recombinant nucleic acid.

The Examiner considers that the term "oleaginous" in claim 19 is indefinite and can relate either to olive trees or to oil. This rejection has been obviated by cancellation of claim 19.

Furthermore, the Examiner purports that claims 32 to 34 are indefinite in the recitation of the expression "promoter region." Indeed, the Examiner considers that the expression "promoter region" is unclear since this means all or part of the sequence that functions to promote transcription. Applicants have amended the above rejected claims to replace the expression "promoter region" by the term "promoter", which should render moot the Examiner's rejection.

In view of the above, withdrawal of this rejection is respectfully requested.

Claims 1, 2, 12, 13, 17 to 21, 23, 30 and 31 to 34 have been rejected under 35 U.S.C. §112, first paragraph, as containing subject matter which was not described in the specification in such a way as to convey to one skilled in the art, at the time the application was filed, that the inventors had possession of the claimed invention. This rejection has been rendered moot in part by the amended claim 1 and traversed by the following explanation.

In rendering this rejection, the Examiner deems that the specification discloses only two different types of methyl transferases at least on page 8 lines 20 to 23 and page 7 lines 18 to 20 and fails to sufficiently describe a representative number of methyl transferase genes.

According to the Guidelines for examination of patent applications under 35 U.S.C. §112, first paragraph for the satisfactory disclosure, the "representative number" depends on whether one of skill in the art would recognize that the Applicants were in possession of the necessary common features of the genus of methyl transferase genes but does not require an individual support for each said methyl transferase genes catalyzing the transfer of a methyl group to an aliphatic chain of an unsaturated fatty acid.

First of all, the specification of the present application clearly describes methyl transferase genes such as cyclopropane fatty acid synthase (Wang et al.

Biochemistry 31, 1992) , methyl transferase responsible for the synthesis of 9-methyl-10-hexadecenoic acid in Corynebacterium (Niepel et al. J. Bact. 180, 1998) and in a variety of alga (Carballeira et al. Lipids 32, 1997) at least on page 7 of the description.

Furthermore, the description discloses, at least on page 21 lines 1 to 7 and page 8 lines 5 to 19, selection and isolation of the nucleic acids coding for methyl transferase enzymes. Nucleic acid sequences are derived from prokaryotic and eukaryotic organisms and their coding sequences are analogues of the coding sequence of the previous examples described by Wang et al., Niepel et al. and Carballaira et al.

Secondly, methyl transferase genes as described in the present invention have at least a common feature consisting in catalyzing the transfer of a methyl group to an aliphatic chain of an unsaturated fatty acid. Applicants deem that the two methyl transferase genes, i.e., SAM-methyl transferase and cyclopropane fatty acid synthase gene (CFAS) precisely described in the specification and tested in the transformed plants disclosed at least on page 19 and following (example A), adequately describe the common feature of the methyl transferase genes of the amended claim 1 consisting in catalyzing the transfer of a methyl group to an aliphatic chain of an unsaturated fatty acid.

Therefore in view of the above, the description should reasonably convey to one skilled in the art that the inventors had possession of the claimed invention at the time the application was filed.

Therefore, withdrawal of this rejection is respectfully requested.

Claims 1, 2, 12, 13, 17 to 21, 30 and 31 have been rejected under 35 U.S.C. § 112, first paragraph, for lack of enablement. For the following reasons, this rejection is respectfully traversed.

It should be recalled that the Examiner purports that the specification is only enabling for cyclopropane fatty acid synthase, which is a methyltransferase, in tobacco plants. The Examiner has substantiated her reasons for this enablement

rejection by relying on three articles and has concluded that the art is unpredictable. However, Applicants respectfully submit that the Examiner has not met her burden of providing sound reasons why the claims are not enabled since the references that the Examiner has relied on are not at all related to the specifically claimed invention.

First of all, the articles of Van de Loo et al and Broun et al, cited by the Examiner in maintaining this rejection are directed to fatty acid hydroxylases. It is well known in this art that hydroxylases catalyze the **introduction of one or more hydroxyl groups** into a compound by the replacement of hydrogen atom(s). Fatty acid hydroxylases catalyze an entirely different reaction than that of methyltransferases. Indeed, it is well known in this art that methyltransferases are enzymes that catalyze **the transfer of a methyl group** into a compound.

Thus, the reaction that is catalyzed using the methyltransferase enzyme is totally different than the art cited by the Examiner, which art describes a totally different enzymatic reaction. Applicants submit that the Examiner cannot equate the teachings of the fatty acid hydroxylase art with that of the methyltransferase art as being similar.

Furthermore, with respect to the Examiner's reliance on the reference of De Luca to reach the conclusion that the field of the present invention is highly unpredictable cannot be maintained. Indeed, De Luca concerns the molecular characterization of **secondary metabolic pathways**. Secondary metabolic pathways are known in the art as those pathways which **are not essential for cell viability** but nevertheless play an important role in the survival and fitness of the whole plant.

The present invention is concerned with a method for the production of branched chained fatty acids. Fatty acid production is not considered as a secondary metabolic pathway, but a **primary metabolic pathway**, since it is needed to keep **the cells alive**.

Indeed, DeLuca emphasize that the unpredictability of using transgenic plant technology is not associated with the unpredictability of producing transgenic plants *per se*, but lies in the unpredictability concerning the poor understanding of plant secondary metabolic pathways and their *in vivo* regulation. See, page 225N, second column.

In contrast, in the present invention the fatty acid metabolic pathway was well known in the art at the time of filing of the present invention. This fact is evidenced by the attached section of Biochemistry by Lehninger which was copyrighted in 1977, 30 years prior to the priority date of the present invention.

Therefore, the cited references cannot be relied upon by the Examiner as providing a reasonable explanation as to why the claims of the present invention are not adequately enabled by the description, since these references are not even closely associated with the present invention. A reasonable explanation is necessary by law to maintain an enablement rejection.

Furthermore, the Examiner has not provided any explanation as to why plants other than tobacco plants can be transformed using the teachings of the specification. It should be noted that genetic engineering of plants has been successfully accomplished since about 1983. There is no unpredictability in this field.

Finally, the Examiner deems that the teachings in the specification concerning methyltransferases are only prophetic. Applicants respectfully disagree since the examples of the specification are directed towards cyclopropane fatty acid synthase, which is a methyltransferase.

In conclusion, Applicants submit that the Examiner has not provided sufficient reasonable explanations as to why the scope of protection in the claims is not adequately enabled by the description. This burden has not been met and therefore, this rejection cannot be legally maintained. See, *In re Wright*, 999 F.2d 1557, 1561-1562, 27 USPQ2d 1510, 1513 (Fed. Cir. 1993).

Thus, in view of the above, withdrawal of this rejection is respectfully requested.

Claims 12, 13, 17, 18 and 34 have been rejected under 35 U.S.C. § 102 (e) as being anticipated by Fritig et al. (US Patent 5,959,178). In rendering this rejection the Examiner purports that Fritig et al. teach a recombinant nucleic acid comprising a nucleic acid coding for a methyl transferase, a plant expressible promoter and a termination region.

Claim 12 is directed to a nucleic acid coding for a methyl transferase catalyzing the transfer of a methyl group to an aliphatic chain of an unsaturated fatty acid. Fritig et al. disclose a O-methyl transferase (OMT) catalyzing methylation reactions on cinnamic acid. Accordingly, OMT introduces a methyl group on the aromatic ring of the cinnamic acid molecule, said ring is located in position 3 of the propenoic acid consisting this molecule, i.e. "methylation reactions, thus producing different acids substituted on the aromatic ring" as described at column 2 lines 11 to 24. Furthermore, "OMTs introduce one and two methoxy groups in the lignin monomers", which have also a cyclic structure. Hence, Fritig et al. have not disclosed a methyl transferase capable of introducing a methyl group to an aliphatic chain of an unsaturated fatty acid.

Therefore, in view of the above, withdrawal of this rejection is respectfully requested.

From the foregoing, favorable action in the form of a Notice of Allowance is respectfully requested and such action is earnestly solicited.

Respectfully submitted,

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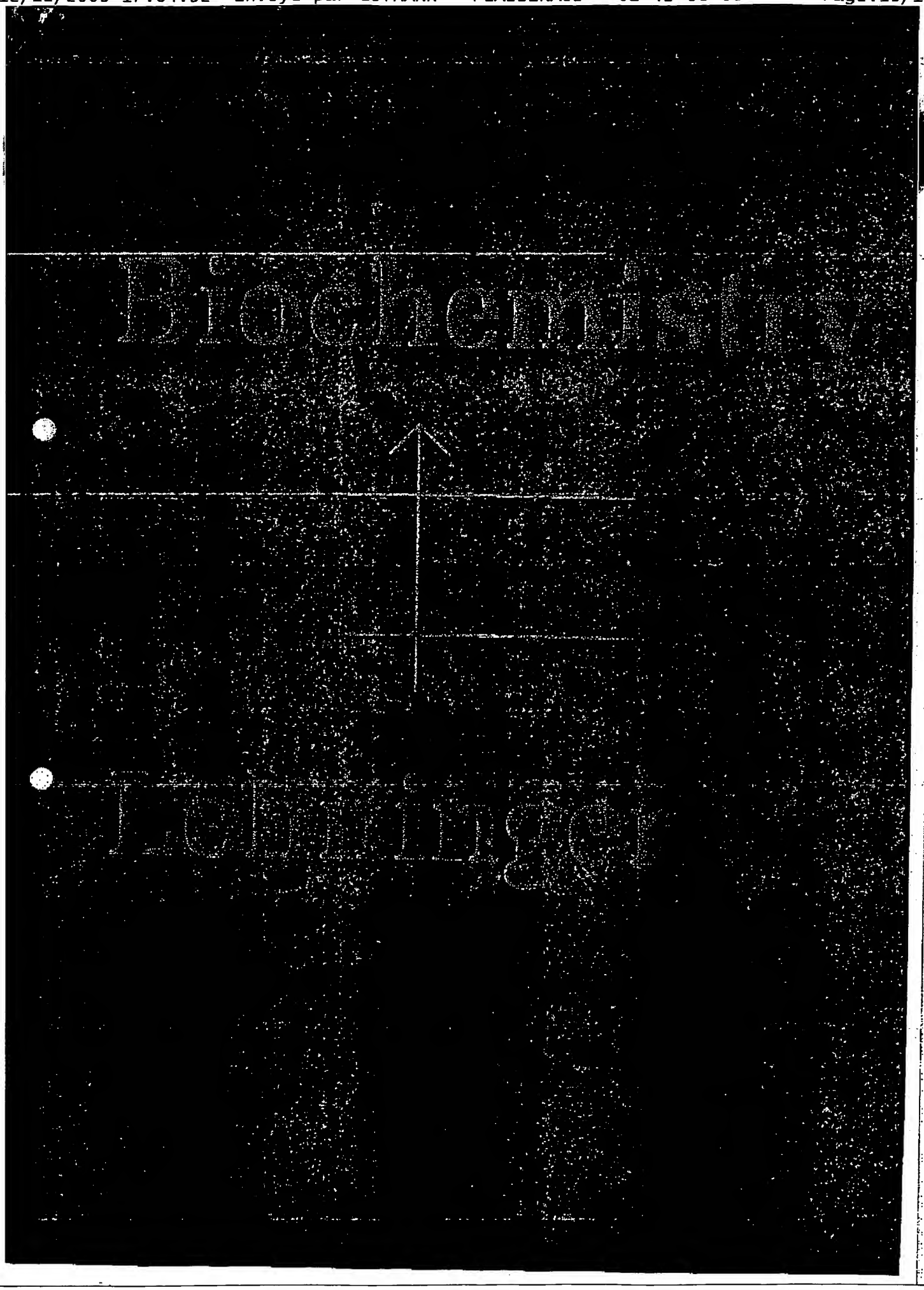
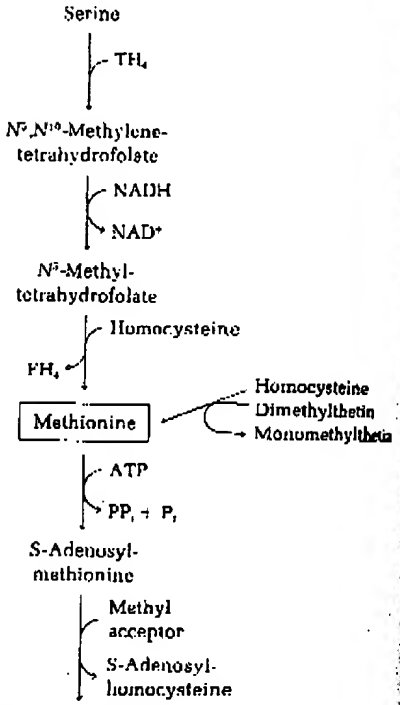

Biochemistry

Table 25-1 Precursor functions of some amino acids

Arginine	Serine
Spermine	Sphingosine
Spermidine	Tyrosine
Putrescine	Epinephrine
Aspartic acid	Norepinephrine
Pyrimidines	Melanin
Glutamic acid	Thyroxine
Glutathione	Mescaline
Glycine	Tyramine
Purines	Morphine
Glutathione	Codeine
Creatine	Papaverine
Phosphocreatine	Tryptophan
Tetrapyrroles	Nicotinic acid
Histidine	Serotonin
Histamine	Kynurenic acid
Ergothioneine	Indole
Lysine	Skatole
Cadaverine	Indoleacetic acid
Anabasine	Ommochrome
Coniine	Valine
Ornithine	Pantothenic acid
Hyoscyamine	Penicillin

Figure 25-19
The origin and pathway of transfer of methyl groups. Nearly all biological methylation processes in higher animals (and probably most of those in plants and bacteria) involve methionine as the key intermediate. Plants and bacteria manufacture methionine from homocysteine and serine, the major source of the methyl group. S-Adenosylmethionine is the major methyl-group donor to a large number of methyl acceptors. Betaine and dimethylthetin are active donors of methyl groups to homocysteine in some microorganisms.



Methylated acceptors:

Creatine
Phosphatidylcholine
Epinephrine
Cyclic fatty acids
Ergosterol
Vitamin B_{12}
N-Methylhistamine
N-Methylnicotinamide
Choline
Sarcosine
Anserine

S-Adenosylmethionine is the direct methyl-group donor to some 40 different methyl-group acceptors, of which a partial list is given in Figure 25-19. Such transfers are catalyzed by *methyltransferases*, which yield S-adenosylhomocysteine as the demethylated product.

Although methionine serves as a general methyl-group donor to many methyl-group acceptors, the formation of the methyl group of methionine occurs by only a very few reactions. The major pathway is by transfer of a methyl group from N^5-methyltetrahydrofolate to homocysteine (Figure 25-19). The methyl group of N^5-methyltetrahydrofolate in turn derives from a limited number of metabolites capable of donating one-carbon functional groups to tetrahydrofolate, particularly serine. The sources of one-carbon groups and other aspects of their metabolism are discussed elsewhere (pages 345, 567, and 731).

Peptides

Amino acids are biological precursors of a number of peptides, many of which, such as the hormones oxytocin, vasopressin, and bradykinin (page 96), have intense biological activity.

The simple tripeptide *glutathione* of animal tissues (Figure 25-20), which serves as a component of an amino acid transport system (page 795), an activator of certain enzymes, and in the protection of lipids against autoxidation, is syn-

For Jan

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